add the canceled claims and subject matter to currently pending and co-owned case USSN 08/441,443. If applicant's request to add the proposed canceled claims and subject matter to USSN 08/441,443 is denied, then applicants withdraw their conditional authorization for the Examiner's amendment proposed herein and the claims as pending December 24, 2002, should remain. For the Examiner's convenience, applicants herein submit three sets of claims: 1) the claims currently pending; 2) a marked-up claim set with the proposed Examiner's amendment and; 3) the claims following the proposed Examiner's amendment. The Examiner is conditionally authorized to amend claims 118, 119, 132, 138 and 144 as follows:

118. (Twice Amended) A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. (Twice Amended) A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

132. (Amended) A method according to any of claims 118, 119 and 123-125, wherein said biological samples are blood.

138. (Amended) A method according to any of claims 118, 119 and 123-125, wherein said biological samples are plasma.

144. (Amended) A method according to any of claims 118, 119 and 123-125, wherein said biological samples are sera.

Double Patenting Rejections

Claims 118, 119, 123-125, 129-132, 136-138, 142-144, 148-150, 152, 158, 160, 161, 164, 169, 170, 171, 175-177, 181, 182 and 183-344 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-41 of U.S. Patent No. 5,350,671.

Applicants respectfully traverse this rejection and its supporting remarks. If the proposed Examiner's amendment is entered, claims 220-282 will be canceled. Nevertheless, in order to advance prosecution, Applicants herewith submit a terminal disclaimer in order to obviate the obvious-type double patenting rejection of claims 118, 119, 123-125, 129-132, 136-138, 142-144, 148-150, 152, 158, 160-161, 164, 169-171, 175-177, 181-219 and 283-344 over claims 1-41 of U.S. Patent No. 5,350,671.

Claims 115-122, 126, 127, 128, 132-135, 138-141, 144-147, 151-153, 158-160, 162-166, 168, 171-174, 177-180 and 183-344 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-6 of U.S. Patent No. 5,863,719.

Applicants respectfully traverse this rejection and its supporting arguments. If the proposed Examiner's amendment is entered, claims 115-117, 120-122, 126-128, 133-135, 139-141, 151, 153, 159, 162-163, 165, 168, 172-174, 178-180 and 220-282 will be cancelled and claims 118, 119, 132, 138 and 144 will be amended. The obviousness-type double patenting rejection should then be withdrawn.

Claims 118, 119, 123-125, 129-132, 136-138, 142-144, 148-150, 152, 158, 160, 161, 164, 169, 170, 171, 175-177, 181, 182 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-64 of U.S. Patent No. 5,698,390.

Applicants respectfully traverse this rejection and its supporting remarks. If the proposed Examiner's amendment is entered, claims 220-282 will be canceled. Nevertheless, in order to advance prosecution, Applicants herewith submit a terminal disclaimer in order to obviate the

obvious-type double patenting rejection of claims 118, 119, 123-125, 129-132, 136-138, 142-144, 148-150, 152, 158, 160-161, 164, 169-171, 175-177, 181 and 182 over claims 1-64 of U.S. Patent No. 5,698,390.

CONCLUSION

Applicants earnestly believe that they are entitled to a letters patent on the pending claims, and respectfully solicit the Examiner to expedite prosecution of this patent application to issuance. Should the Examiner have any questions, the Examiner is encouraged to telephone the undersigned. If the Examiner determines that the claims are not allowable, Applicants request an opportunity to interview the Examiner.

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 03-1664** referencing docket no. PP00063.021. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: 24 June 2003

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CLAIMS PENDING AS OF DECEMBER 24, 2002 OFFICE ACTION

1-114 Cancelled.

115. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 3.

116 A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 62A.

117. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides fully complementary to either strand of Figure 89.

118. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof, or (ii) antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise either (i) a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394 or (ii) antibodies that form an antigen-antibody complex

with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

120. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 89.

121. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides found in either strand of Figure 14.

122. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

123. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

124. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 14.

125. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with a hepatitis C virus (HCV) polypeptide sequence of at least 10

contiguous amino acid encoded by an HCV cDNA insert in a lambda gt-11 library deposited as ATCC deposit No. 40394.

126. A method according to any of claims 118-122 wherein said selected samples comprise said polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said polynucleotide and said contiguous sequence and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

127. A method according to any of claims 115-122, 162 or 163 wherein said polynucleotide is detectable in a PCR assay.

128. A method according to claim 126 wherein said polynucleotide is detectable in a PCR assay.

129. A method according to any of claims 118, 119, and 123-125 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

130. A method according to claim 129 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

131. A method according to claim 130 wherein said antigen is a fusion protein.

132. A method according to any of claims 115-125, 162 or 163 wherein said biological samples are blood .

133. A method according to claim 126 wherein said biological samples are blood.

134. A method according to claim 127 wherein said biological samples are blood.

135. A method according to claim 128 wherein said biological samples are blood.

136. A method according to claim 129 wherein said biological samples are blood.

137. A method according to claim 130 wherein said biological samples are blood.

138. A method according to any of claims 115-125, 162 or 163 wherein said biological samples are plasma.

139. A method according to claim 126 wherein said biological samples are plasma.

140. A method according to claim 127 wherein said biological samples are plasma.

141. A method according to claim 128 wherein said biological samples are plasma.

142. A method according to claim 129 wherein said biological samples are plasma.

143. A method according to claim 130 wherein said biological samples are plasma.

144. A method according to any of claims 115-125, 162 or 163 wherein said biological samples are sera.

145. A method according to claim 126 wherein said biological samples are sera.

146. A method according to claim 127 wherein said biological samples are sera.

147. A method according to claim 128 wherein said biological samples are sera.

148. A method according to claim 129 wherein said biological samples are sera.

149. A method according to claim 130 wherein said biological samples are sera.

150. A method according to claim 132 further comprising employing biological samples that are not selected for a preparation of blood-related products.

151. A method according to claim 133 further comprising employing biological samples that are not selected for a preparation of blood-related products.

152. A method according to claim 138 further comprising employing biological samples that are not selected for a preparation of blood-related products.

153. A method according to claim 139 further comprising employing biological samples that are not selected for a preparation of blood-related products.

154-157 Cancelled.

158. A method according to claim 132 further comprising preparing polyclonal antibodies with the selected biological samples.

159. A method according to claim 133 further comprising preparing polyclonal antibodies with the selected biological samples.

160. A method according to claim 138 further comprising preparing polyclonal antibodies with the selected biological samples.

161. A method according to claim 142 further comprising preparing polyclonal antibodies with the selected biological samples.

162. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

163. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a sequence that is fully complementary to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

164. A method according to claim 132 wherein the selecting is to identify an HCV positive sample for removal from the supply.

165. A method according to claim 133 wherein the selecting is to identify an HCV positive sample for removal from the supply.

166. A method according to claim 134 wherein the selecting is to identify an HCV positive sample for removal from the supply.

167. Cancelled.

168. A method according to claim 135 wherein the selecting is to identify an HCV positive sample for removal from the supply.

169. A method according to claim 136 wherein the selecting is to identify an HCV positive sample for removal from the supply.

170. A method according to claim 137 wherein the selecting is to identify an HCV positive sample for removal from the supply.

171. A method according to claim 138 wherein the selecting is to identify an HCV positive sample for removal from the supply.

172. A method according to claim 139 wherein the selecting is to identify an HCV positive sample for removal from the supply.

173. A method according to claim 140 wherein the selecting is to identify an HCV positive sample for removal from the supply.

174. A method according to claim 141 wherein the selecting is to identify an HCV positive sample for removal from the supply.

175. A method according to claim 142 wherein the selecting is to identify an HCV positive sample for removal from the supply.

176. A method according to claim 143 wherein the selecting is to identify an HCV positive sample for removal from the supply.

177. A method according to claim 144 wherein the selecting is to identify an HCV positive sample for removal from the supply.

178. A method according to claim 145 wherein the selecting is to identify an HCV positive sample for removal from the supply.

179. A method according to claim 146 wherein the selecting is to identify an HCV positive sample for removal from the supply.

180. A method according to claim 147 wherein the selecting is to identify an HCV positive sample for removal from the supply.

181. A method according to claim 148 wherein the selecting is to identify an HCV positive sample for removal from the supply.

182. A method according to claim 149 wherein the selecting is to identify an HCV positive sample for removal from the supply.

183. A method according to any one of claims 123, 124 or 125, wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 15 contiguous amino acids.

184. The method according to claim 118 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by a hepatitis C virus genome.

185. The method according to claim 119 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

186. The method according to claim 123 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 90.

187. The method according to claim 124 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 14.

188. The method according to claim 125 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than

about 100 contiguous amino acids encoded by an HCV cDNA insert in a lambda gt-11 library deposited as ATCC deposit No. 40394.

189. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA50; AA1-AA84; AA9-AA177; AA1-AA120; AA35-AA45; AA50-AA100; AA40-AA90; AA65-AA75; AA80-AA90; AA99-AA120; AA95-AA110; AA100-AA150; AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-AA330; AA290-AA305; AA300-AA-350; AA310-AA330; AA350-AA400;AA405-AA495; AA400-AA450; AA437-AA582; AA450-AA500; AA475-AA495;AA500-AA550; AA511-AA690; AA515-AA550; AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625; AA635-AA665; AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775; AA770-AA790; AA750-AA800; AA800-AA815; AA850-AA875; AA800-AA850; AA920-AA990; AA850-AA900; AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100; AA1100-AA1140; AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250; AA1250-AA1300; AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350; AA1310-AA1340; AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405; AA1400-AA1450; AA1450-AA1500; AA1475-AA1515; AA1475-AA1500; AA1500-AA1550; AA1515-AA1550; AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610; AA1590-AA1650; AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805; AA1690-AA1720; AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800; AA1775-AA1810; AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920; AA1916-AA2021; AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985; AA2000-AA2050; AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223; AA2070-AA2100; AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330; AA2265-AA2280; AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400; AA2345-AA2415; AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450; AA2400-AA2425; AA2415-AA2450; AA2445-AA2500; AA2371-AA2502;

AA2500-AA2550; AA2505-AA2540; AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650; AA2650-AA2700; AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800; AA2755-AA2780; AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825; AA2800-AA2850; AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950;

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

190. The method according to claim 189 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

191. The method according to claim 190 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

192. The method according to claim 190 wherein said biological samples are blood.

193. The method according to claim 191 wherein said biological samples are blood.

194. The method according to claim 190 wherein said biological samples are plasma.

195. The method according to claim 191 wherein said biological samples are plasma.

196. The method according to claim 190 wherein said biological samples are sera.

197. The method according to claim 191 wherein said biological samples are sera.

198. The method according to claim 192 wherein the selecting is to identify an HCV positive sample for removal from the supply.

199. The method according to claim 193 wherein the selecting is to identify an HCV positive sample for removal from the supply.

200. The method according to claim 194 wherein the selecting is to identify an HCV positive sample for removal from the supply.

201. The method according to claim 195 wherein the selecting is to identify an HCV positive sample for removal from the supply.

202. The method according to claim 196 wherein the selecting is to identify an HCV positive sample for removal from the supply.

203. The method according to claim 197 wherein the selecting is to identify an HCV positive sample for removal from the supply.

204. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA84; AA437-AA582; AA511-AA690; AA9-AA177; AA1192-AA1457; AA1266-AA1428; AA1694-AA1735; AA1689-AA1805; AA1916-AA2021; AA1949-AA2124; AA2054-AA2223; AA2200-AA3325; AA2287-AA2385; AA2348-AA2464; AA2371-AA2502; AA2796-AA2886; AA1569-AA1931,

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

205. The method according to claim 204 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

206. The method according to claim 205 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

207. The method according to claim 205 wherein said biological samples are blood.

208. The method according to claim 206 wherein said biological samples are blood.

209. The method according to claim 205 wherein said biological samples are plasma.

210. The method according to claim 206 wherein said biological samples are plasma.

211. The method according to claim 205 wherein said biological samples are sera.

212. The method according to claim 206 wherein said biological samples are sera.

213. The method according to claim 207 wherein the selecting is to identify an HCV positive sample for removal from the supply.

214. The method according to claim 208 wherein the selecting is to identify an HCV positive sample for removal from the supply.

215. The method according to claim 209 wherein the selecting is to identify an HCV positive sample for removal from the supply.

216. The method according to claim 210 wherein the selecting is to identify an HCV positive sample for removal from the supply.

217. The method according to claim 211 wherein the selecting is to identify an HCV positive sample for removal from the supply.

218. The method according to claim 212 wherein the selecting is to identify an HCV positive sample for removal from the supply.

219. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1694-AA1735; AA1569-AA1931; AA1192-AA1457; AA1-AA84; and AA9-AA177, wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x

and y denoting amino acid numbers of HCV-1 polyprotein or corresponding regions of other HCV isolates.

220. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

221. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

222. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

223. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

224. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in Figure 89, or the complement thereof.

225. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in Figure 89, or the complement thereof.

226. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in either strand of Figure 58.

227. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in either stand of Figure 58.

228. A method according to any of claims 220, 222, 224, or 226 wherein said selected samples comprise said first polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said first polynucleotide and said contiguous sequence of nucleotides and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

229. A method according to any of claims 221, 223, 225 or 227 wherein said selected samples do not comprise said first polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said first polynucleotide and said contiguous sequence and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

230. A method according to claim 228, wherein said stringent conditions include using 50% (w/v) formamide and washing in 5xSSC, 0.1% SDS at 55 °C.

231. A method according to claim 229, wherein said stringent conditions include using 50% (w/v) formamide and washing in 5xSSC, 0.1% SDS at 55 °C.

232. A method according to claim 228 wherein said first polynucleotide is detectable in a PCR assay.

233. A method according to 230, wherein said first polynucleotide is detectable in a PCR assay.

234. A method according to claim 229 wherein said first polynucleotide is not detectable in a PCR assay.

235. A method according to claim 231 wherein said first polynucleotide is not detectable in a PCR assay.

236. A method according to any of claims 220-227 wherein said biological samples are blood.

237. A method according to claim 228 wherein said biological samples are blood.

238. A method according to claim 229 wherein said biological samples are blood.

239. A method according to claim 230 wherein said biological samples are blood.

240. A method according to claim 231 wherein said biological samples are blood.

241. A method according to claim 232 wherein said biological samples are blood.

242. A method according to claim 233 wherein said biological samples are blood.

243. A method according to claim 234 wherein said biological samples are blood.

244. A method according to claim 235 wherein said biological samples are blood.

245. A method according to any of claims 220-227 wherein said biological samples are plasma.

246. A method according to claim 228 wherein said biological samples are plasma.

247. A method according to claim 229 wherein said biological samples are plasma.

248. A method according to claim 230 wherein said biological samples are plasma.

249. A method according to claim 231 wherein said biological samples are plasma.

250. A method according to claim 232 wherein said biological samples are plasma.

251. A method according to claim 233 wherein said biological samples are plasma.

252. A method according to claim 234 wherein said biological samples are plasma.

253. A method according to claim 235 wherein said biological samples are plasma.

254. A method according to any of claims 220-227 wherein said biological samples are sera.

255. A method according to claim 228 wherein said biological samples are sera.

256. A method according to claim 229 wherein said biological samples are sera.

257. A method according to claim 230 wherein said biological samples are sera.

258. A method according to claim 231 wherein said biological samples are sera.

259. A method according to claim 232 wherein said biological samples are sera.

260. A method according to claim 233 wherein said biological samples are sera.

261. A method according to claim 234 wherein said biological samples are sera.

262. A method according to claim 235 wherein said biological samples are sera.

263. A method according to any of claims 220, 222, 224, or 226 further comprising employing biological samples that are not selected for a preparation of blood-related products.

264. A method according to claim 228 further comprising employing biological samples that are not selected for a preparation of blood-related products.

265. A method according to claim 230 further comprising employing biological samples that are not selected for a preparation of blood-related products.

266. A method according to claim 232 further comprising employing biological samples that are not selected for a preparation of blood-related products.

267. A method according to claim 233 further comprising employing biological samples that are not selected for a preparation of blood-related products.

268. A method according to any of claims 221, 223, 225, or 227 further comprising employing biological samples that are selected for a preparation of blood-related products.

269. A method according to claim 229 further comprising employing biological samples that are selected for a preparation of blood-related products.

270. A method according to claim 231 further comprising employing biological samples that are not selected for a preparation of blood-related products.

271. A method according to claim 234 further comprising employing biological samples that are not selected for a preparation of blood-related products.

272. A method according to claim 235 further comprising employing biological samples that are not selected for a preparation of blood-related products.

273. A method according to any of claims 221, 223, 225 or 227 wherein said selected samples are supply samples for preparation of blood products.

274. A method according to claim 229 wherein said selected samples are supply sample for preparation of blood products.

275. A method according to claim 231 wherein said selected samples are supply sample for preparation of blood products.

276. method according to claim 234 wherein said selected samples are supply sample for preparation of blood products.

277. method according to claim 235 wherein said selected samples are supply sample for preparation of blood products.

278. A method according to any of claims 220, 222, 224 or 226 wherein said samples that are not selected are supply samples for preparation of blood products.

279. A method according to claim 228 wherein said samples that are not selected are supply samples for preparation of blood products.

280. A method according to claim 230 wherein said samples that are not selected are supply samples for preparation of blood products.

281. A method according to claim 232 wherein said samples that are not selected are supply samples for preparation of blood products.

282. A method according to claim 233 wherein said samples that are not selected samples supply samples for preparation of blood products.

283. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

284. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

285. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids

encoded by at least one of the HCV cDNA inserts in a lambda gt-11 library deposited as ATCC Deposit No. 40394.

286. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by at least one of the HCV cDNA inserts in a lambda gt-11 library deposited as ATCC Deposit No. 40394.

287. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

288. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

289. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 62.

290. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 62.

291. A method according to any of claims 283, 285, 287 or 289 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

292. A method according to any of claims 284, 286, 288 or 290 wherein said antibodies are not detectable in an ELISA or radioimmunoassay.

293. A method according to claim 291 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

294. A method according to claim 292 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

295. A method according to claim 293 wherein said antigen is a fusion protein.

296. A method according to claim 294 wherein said antigen is a fusion protein.

297. A method according to any of claims 283-290 wherein said biological samples are blood.

298. A method according to claim 291 wherein said biological samples are blood.

299. A method according to claim 292 wherein said biological samples are blood.

300. A method according to claim 293 wherein said biological samples are blood.

301. A method according to claim 294 wherein said biological samples are blood.

302. A method according to any of claims 283-290 wherein said biological samples are plasma.

303. A method according to claim 291 wherein said biological samples are plasma.

304. A method according to claim 292 wherein said biological samples are plasma.

305. A method according to claim 293 wherein said biological samples are plasma.

306. A method according to claim 294 wherein said biological samples are plasma.

307. A method according to any of claims 283-290 wherein said biological samples are sera.

308. A method according to claim 291 wherein said biological samples are sera.

309. A method according to claim 292 wherein said biological samples are sera.

310. A method according to claim 293 wherein said biological samples are sera.

311. A method according to claim 294 wherein said biological samples are sera.

312. A method according to any of claims 283, 285, 287 or 289 further comprising employing biological samples that are not selected for a preparation of blood-related products.

313. A method according to claim 291 further comprising employing biological samples that are not selected for a preparation of blood-related products.

314. A method according to claim 293 further comprising employing biological samples that are not selected for a preparation of blood-related products.

315. A method according to any of claims 284, 286, 288 or 290 further comprising employing biological samples that are selected for a preparation of blood-related products.

316. A method according to claim 292 further comprising employing biological samples that are selected for a preparation of blood-related products.

317. A method according to claim 294 further comprising employing biological samples that are selected for a preparation of blood-related products.

318. A method according to any of claims 283, 285, 287 or 289 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

319. A method according to claim 291 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

320. A method according to claim 293 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

321. A method according to any of claim 284, 286, 288 or 290 wherein said selected samples are supply samples for preparation of blood products.

322. A method according to claim 292 wherein said selected samples are supply samples for preparation of blood products.

323. A method according to claim 294 wherein said selected samples are supply samples for preparation of blood products.

324. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by a hepatitis C virus genome.

325. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

326. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 90.

327. A method according to any of claims 283, 285, 287 or 289 wherein the contiguous sequence is found within the sequence selected from the group consisting of:

AA1-AA50; AA1-AA84; AA9-AA177; AA1-AA120; AA35-AA45; AA50-AA100; AA40-AA90; AA65-AA75; AA80-AA90; AA99-AA120; AA95-AA110; AA100-AA150; AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-AA330; AA290-AA305; AA300-AA350; AA310-AA330; AA350-AA400; AA405-AA495; AA400-AA450; AA437-AA582; AA450-AA500; AA475-AA495; AA500-AA550; AA511-AA690; AA515-AA550; AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625; AA635-AA665; AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775; AA770-AA790; AA750-AA800; AA800-AA815; AA850-AA875; AA800-

AA850; AA920-AA990; AA850-AA900; AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1000AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100; AA1100-AA1140; AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250; AA1250-AA1300; AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350; AA1310-AA1340; AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405; AA1400-AA1450; AA1450-AA1500; AA1475-AA1500; AA1500-AA1550; AA1515-AA1550; AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610; AA1590-AA1650; AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805; AA1690-AA1720; AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800; AA1775-AA1810; AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920; AA1916-AA2021; AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985; AA2000-AA2050; AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223; AA2070-AA2100; AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330; AA2265-AA2280; AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400; AA2345-AA2415; AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450; AA2400-AA2425; AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550; AA2505-AA2540; AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650; AA2650-AA2700; AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800; AA2755-AA2780; AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825; AA2800-AA2850; AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950,
wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

328. The method according to any of claims 324-327 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

329. The method according to claim 328 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

330. The method according to claim 328 wherein said biological samples are blood.

331. The method according to claim 329 wherein said biological samples are blood.

332. The method according to claim 328 wherein said biological samples are sera.

333. The method according to claim 329 wherein said biological samples are sera.

334. The method according to claim 328 wherein said biological samples are plasma.

335. The method according to claim 329 wherein said biological samples are plasma.

336. A method according to any of claims 324-327 wherein the contiguous sequence is found within the sequence selected from the group consisting of:

AA1-AA84; AA37-AA582; AA511-AA690; AA9-AA177; AA1192-AA1457; AA1266-AA1428; AA1694-AA1735; AA1689-AA1805; AA1916-AA2021; AA1949-AA2124; AA2054-AA2223; AA2200-AA3325; AA2287-AA2385; AA2348-AA2464; AA2371-AA2502; AA2796-AA2886; AA1569-AA1931, wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

337. The method according to claim 336 wherein said antibodies are detectable in an ELISA or radioimmunoasssay.

338. The method according to claim 337 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

339. The method according to claim 337 wherein said biological samples are blood.

340. The method according to claim 338 wherein said biological samples are blood.

341. The method according to claim 337 wherein said biological samples are plasma.

342. The method according to claim 338 wherein said biological samples are plasma.

343. The method according to claim 337 wherein said biological samples are sera.

344. The method according to claim 338 wherein said biological samples are sera.

VERSION WITH MARKINGS TO SHOW CHANGES AS CONDITIONALLY AUTHORIZED

In the claims:

Claims 115-117, 120-122, 126-128, 133-135, 139-141, 145-147, 151, 153, 159, 162-163, 165-166, 168, 172-174, 178-180 and 220-282 have been canceled.

Claims 118, 119, 132, 138 and 144 have been amended as follows:

118. (Twice Amended) A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise ~~either (i) a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof, or (ii)~~ antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. (Twice Amended) A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise ~~either (i) a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394 or (ii)~~ antibodies that form an antigen-antibody complex with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

132. (Amended) A method according to any of claims ~~115~~ 118, 119 and 123-125, ~~162 or 163~~ wherein said biological samples are blood .

138. (Amended) A method according to any of ~~115~~ 118, 119 and 123-125, ~~162 or 163~~ wherein said biological samples are plasma.

144. (Amended) A method according to any of claims ~~115~~ 118, 119 and 123-125, ~~162 or 163~~ wherein said biological samples are sera.

CLAIMS IF EXAMINER'S AMENDMENT IS ENTERED

In the Claims:

1-117 Cancelled.

118. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

119. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an HCV polypeptide sequence of at least 10 contiguous amino acid encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

120-122 Cancelled

123. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

124. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 14.

125. A method of selecting biological samples from a supply of human biological samples comprising selecting from said supply those samples that comprise antibodies that form an antigen-antibody complex with a hepatitis C virus (HCV) polypeptide sequence of at least 10

contiguous amino acid encoded by an HCV cDNA insert in a lambda gt-11 library deposited as ATCC deposit No. 40394.

126-128 Cancelled

129. A method according to any of claims 118, 119, and 123-125 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

130. A method according to claim 129 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

131. A method according to claim 130 wherein said antigen is a fusion protein.

132. A method according to any of claims 118-119, and 123-125, wherein said biological samples are blood.

133-135 Cancelled

136. A method according to claim 129 wherein said biological samples are blood.

137. A method according to claim 130 wherein said biological samples are blood.

138. A method according to any of claims 118-119, and 123-125, wherein said biological samples are plasma.

139-141 Cancelled

142. A method according to claim 129 wherein said biological samples are plasma.

143. A method according to claim 130 wherein said biological samples are plasma.

144. A method according to any of claims 118-119, or 123-125, wherein said biological samples are sera.

145-147 Cancelled

148. A method according to claim 129 wherein said biological samples are sera.

149. A method according to claim 130 wherein said biological samples are sera.

150. A method according to claim 132 further comprising employing biological samples that are not selected for a preparation of blood-related products.

151. Cancelled

152. A method according to claim 138 further comprising employing biological samples that are not selected for a preparation of blood-related products.

153-157 Cancelled.

158. A method according to claim 132 further comprising preparing polyclonal antibodies with the selected biological samples.

159. Cancelled

160. A method according to claim 138 further comprising preparing polyclonal antibodies with the selected biological samples.

161. A method according to claim 142 further comprising preparing polyclonal antibodies with the selected biological samples.

162-163 Cancelled

164. A method according to claim 132 wherein the selecting is to identify an HCV positive sample for removal from the supply.

165-168 Cancelled

169. A method according to claim 136 wherein the selecting is to identify an HCV positive sample for removal from the supply.

170. A method according to claim 137 wherein the selecting is to identify an HCV positive sample for removal from the supply.

171. A method according to claim 138 wherein the selecting is to identify an HCV positive sample for removal from the supply.

172-174 Cancelled

175. A method according to claim 142 wherein the selecting is to identify an HCV positive sample for removal from the supply.

176. A method according to claim 143 wherein the selecting is to identify an HCV positive sample for removal from the supply.

177. A method according to claim 144 wherein the selecting is to identify an HCV positive sample for removal from the supply.

178-180 Cancelled

181. A method according to claim 148 wherein the selecting is to identify an HCV positive sample for removal from the supply.

182. A method according to claim 149 wherein the selecting is to identify an HCV positive sample for removal from the supply.

183. A method according to any one of claims 123, 124 or 125, wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 15 contiguous amino acids.

184. The method according to claim 118 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by a hepatitis C virus genome.

185. The method according to claim 119 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

186. The method according to claim 123 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 90.

187. The method according to claim 124 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 14.

188. The method according to claim 125 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in a lambda gt-11 library deposited as ATCC deposit No. 40394.

189. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA50; AA1-AA84; AA9-AA177; AA1-AA120; AA35-AA45; AA50-AA100; AA40-AA90; AA65-AA75; AA80-AA90; AA99-AA120; AA95-AA110; AA100-AA150; AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-AA330; AA290-AA305; AA300-AA-350; AA310-AA330; AA350-AA400;AA405-AA495; AA400-AA450; AA437-AA582; AA450-AA500; AA475-AA495;AA500-AA550; AA511-AA690; AA515-AA550; AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625; AA635-AA665; AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775; AA770-AA790; AA750-AA800; AA800-AA815; AA850-AA875; AA800-AA850; AA920-AA990; AA850-AA900; AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100; AA1100-AA1140; AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250; AA1250-AA1300; AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350; AA1310-AA1340; AA1345-AA1405; AA1350-AA1400; AA1365-AA1380;

AA1380-AA1405; AA1400-AA1450; AA1450-AA1500; AA1475-AA1515; AA1475-AA1500; AA1500-AA1550; AA1515-AA1550; AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610; AA1590-AA1650; AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805; AA1690-AA1720; AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800; AA1775-AA1810; AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920; AA1916-AA2021; AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985; AA2000-AA2050; AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223; AA2070-AA2100; AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330; AA2265-AA2280; AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400; AA2345-AA2415; AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450; AA2400-AA2425; AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550; AA2505-AA2540; AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650; AA2650-AA2700; AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800; AA2755-AA2780; AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825; AA2800-AA2850; AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950;

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

190. The method according to claim 189 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

191. The method according to claim 190 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

192. The method according to claim 190 wherein said biological samples are blood.

193. The method according to claim 191 wherein said biological samples are blood.

194. The method according to claim 190 wherein said biological samples are plasma.

195. The method according to claim 191 wherein said biological samples are plasma.

196. The method according to claim 190 wherein said biological samples are sera.

197. The method according to claim 191 wherein said biological samples are sera.

198. The method according to claim 192 wherein the selecting is to identify an HCV positive sample for removal from the supply.

199. The method according to claim 193 wherein the selecting is to identify an HCV positive sample for removal from the supply.

200. The method according to claim 194 wherein the selecting is to identify an HCV positive sample for removal from the supply.

201. The method according to claim 195 wherein the selecting is to identify an HCV positive sample for removal from the supply.

202. The method according to claim 196 wherein the selecting is to identify an HCV positive sample for removal from the supply.

203. The method according to claim 197 wherein the selecting is to identify an HCV positive sample for removal from the supply.

204. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA84; AA437-AA582; AA511-AA690; AA9-AA177; AA1192-AA1457; AA1266-AA1428; AA1694-AA1735; AA1689-AA1805; AA1916-AA2021; AA1949-AA2124; AA2054-AA2223; AA2200-AA3325; AA2287-AA2385; AA2348-AA2464; AA2371-AA2502; AA2796-AA2886; AA1569-AA1931,

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

205. The method according to claim 204 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

206. The method according to claim 205 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

207. The method according to claim 205 wherein said biological samples are blood.

208. The method according to claim 206 wherein said biological samples are blood.

209. The method according to claim 205 wherein said biological samples are plasma.

210. The method according to claim 206 wherein said biological samples are plasma.

211. The method according to claim 205 wherein said biological samples are sera.

212. The method according to claim 206 wherein said biological samples are sera.

213. The method according to claim 207 wherein the selecting is to identify an HCV positive sample for removal from the supply.

214. The method according to claim 208 wherein the selecting is to identify an HCV positive sample for removal from the supply.

215. The method according to claim 209 wherein the selecting is to identify an HCV positive sample for removal from the supply.

216. The method according to claim 210 wherein the selecting is to identify an HCV positive sample for removal from the supply.

217. The method according to claim 211 wherein the selecting is to identify an HCV positive sample for removal from the supply.

218. The method according to claim 212 wherein the selecting is to identify an HCV positive sample for removal from the supply.

219. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1694-AA1735; AA1569-AA1931; AA1192-AA1457; AA1-AA84; and AA9-AA177, wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers of HCV-1 polyprotein or corresponding regions of other HCV isolates.

220-282 Cancelled

283. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

284. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by a hepatitis C virus genome.

285. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids

encoded by at least one of the HCV cDNA inserts in a lambda gt-11 library deposited as ATCC Deposit No. 40394.

286. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids encoded by at least one of the HCV cDNA inserts in a lambda gt-11 library deposited as ATCC Deposit No. 40394.

287. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

288. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 90.

289. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 62.

290. A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise antibodies that form an antigen-antibody complex with an amino acid sequence of at least 10 contiguous amino acids found in Figure 62.

291. A method according to any of claims 283, 285, 287 or 289 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

292. A method according to any of claims 284, 286, 288 or 290 wherein said antibodies are not detectable in an ELISA or radioimmunoassay.

293. A method according to claim 291 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

294. A method according to claim 292 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

295. A method according to claim 293 wherein said antigen is a fusion protein.

296. A method according to claim 294 wherein said antigen is a fusion protein.

297. A method according to any of claims 283-290 wherein said biological samples are blood.

298. A method according to claim 291 wherein said biological samples are blood.

299. A method according to claim 292 wherein said biological samples are blood.

300. A method according to claim 293 wherein said biological samples are blood.

301. A method according to claim 294 wherein said biological samples are blood.

302. A method according to any of claims 283-290 wherein said biological samples are plasma.

303. A method according to claim 291 wherein said biological samples are plasma.

304. A method according to claim 292 wherein said biological samples are plasma.

305. A method according to claim 293 wherein said biological samples are plasma.

306. A method according to claim 294 wherein said biological samples are plasma.

307. A method according to any of claims 283-290 wherein said biological samples are sera.

308. A method according to claim 291 wherein said biological samples are sera.

309. A method according to claim 292 wherein said biological samples are sera.

310. A method according to claim 293 wherein said biological samples are sera.

311. A method according to claim 294 wherein said biological samples are sera.

312. A method according to any of claims 283, 285, 287 or 289 further comprising employing biological samples that are not selected for a preparation of blood-related products.

313. A method according to claim 291 further comprising employing biological samples that are not selected for a preparation of blood-related products.

314. A method according to claim 293 further comprising employing biological samples that are not selected for a preparation of blood-related products.

315. A method according to any of claims 284, 286, 288 or 290 further comprising employing biological samples that are selected for a preparation of blood-related products.

316. A method according to claim 292 further comprising employing biological samples that are selected for a preparation of blood-related products.

317. A method according to claim 294 further comprising employing biological samples that are selected for a preparation of blood-related products.

318. A method according to any of claims 283, 285, 287 or 289 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

319. A method according to claim 291 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

320. A method according to claim 293 wherein said selected samples are supply samples for preparation of polyclonal antibodies.

321. A method according to any of claim 284, 286, 288 or 290 wherein said selected samples are supply samples for preparation of blood products.

322. A method according to claim 292 wherein said selected samples are supply samples for preparation of blood products.

323. A method according to claim 294 wherein said selected samples are supply samples for preparation of blood products.

324. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by a hepatitis C virus genome.

325. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

326. The method according to any of claims 283, 285, 287 or 289 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 90.

327. A method according to any of claims 283, 285, 287 or 289 wherein the contiguous sequence is found within the sequence selected from the group consisting of:

AA1-AA50; AA1-AA84; AA9-AA177; AA1-AA120; AA35-AA45; AA50-AA100; AA40-AA90; AA65-AA75; AA80-AA90; AA99-AA120; AA95-AA110; AA100-AA150; AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-AA330; AA290-AA305; AA300-AA350; AA310-AA330; AA350-AA400; AA405-AA495; AA400-AA450; AA437-AA582; AA450-AA500; AA475-AA495; AA500-AA550; AA511-AA690; AA515-AA550; AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625; AA635-AA665; AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775; AA770-AA790; AA750-AA800; AA800-AA815; AA850-AA875; AA800-

AA850; AA920-AA990; AA850-AA900; AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1000AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100; AA1100-AA1140; AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250; AA1250-AA1300; AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350; AA1310-AA1340; AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405; AA1400-AA1450; AA1450-AA1500; AA1475-AA1500; AA1500-AA1550; AA1515-AA1550; AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610; AA1590-AA1650; AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805; AA1690-AA1720; AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800; AA1775-AA1810; AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920; AA1916-AA2021; AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985; AA2000-AA2050; AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223; AA2070-AA2100; AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330; AA2265-AA2280; AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400; AA2345-AA2415; AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450; AA2400-AA2425; AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550; AA2505-AA2540; AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650; AA2650-AA2700; AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800; AA2755-AA2780; AA2780-AA2830; AA2785-AA2810; AA2796-AA2886; AA2810-AA2825; AA2800-AA2850; AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950,
wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

328. The method according to any of claims 324-327 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

329. The method according to claim 328 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

330. The method according to claim 328 wherein said biological samples are blood.

331. The method according to claim 329 wherein said biological samples are blood.

332. The method according to claim 328 wherein said biological samples are sera.

333. The method according to claim 329 wherein said biological samples are sera.

334. The method according to claim 328 wherein said biological samples are plasma.

335. The method according to claim 329 wherein said biological samples are plasma.

336. A method according to any of claims 324-327 wherein the contiguous sequence is found within the sequence selected from the group consisting of:

AA1-AA84; AA37-AA582; AA511-AA690; AA9-AA177; AA1192-AA1457; AA1266-AA1428; AA1694-AA1735; AA1689-AA1805; AA1916-AA2021; AA1949-AA2124; AA2054-AA2223; AA2200-AA3325; AA2287-AA2385; AA2348-AA2464; AA2371-AA2502; AA2796-AA2886; AA1569-AA1931, wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

337. The method according to claim 336 wherein said antibodies are detectable in an ELISA or radioimmunoasssay.

338. The method according to claim 337 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

339. The method according to claim 337 wherein said biological samples are blood.

340. The method according to claim 338 wherein said biological samples are blood.

341. The method according to claim 337 wherein said biological samples are plasma.

342. The method according to claim 338 wherein said biological samples are plasma.

343. The method according to claim 337 wherein said biological samples are sera.

344. The method according to claim 338 wherein said biological samples are sera.